



## **RAW SEQUENCE LISTING** **ERROR REPORT**

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Application Serial Number: 09/995,419

Source: 01PE

Date Processed by STIC: 12/5/01

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OIKE

## RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/995,419

TIME: 10:02:21

Input Set : A:\096,004 - SeqList.ST25.txt

Output Set: N:\CRF3\11212001\I995419.raw

**Does Not Comply  
Corrected Diskette Needed**

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5     Gold, Joseph D.
6     Schiff, J. Michael
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10 <130> FILE REFERENCE: 096,004 - SeqList
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13 <141> CURRENT FILING DATE: 2001-11-26
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16 <151> PRIOR FILING DATE: 2000-11-27
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Input Set : A:\096,004 - SeqList.ST25.txt

Output Set: N:\CRF3\11212001\I995419.raw

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366	actacctgca	ggcccgaaaa	gtaatccagg	ggttctggga	agaggcgggc	aggagggtca	10200
368	gaggggggca	gcctcaggac	gatggaggca	gtcagtctga	ggctgaaaag	ggagggaggg	10260
370	cctcgagccc	aggcctgcaa	gcgcctccag	aagctggaaa	aagcggggaa	gggacctcc	10320
372	acggagcctg	cagcaggaag	gcacggctgg	cccttagccc	accaggggccc	atcgtggacc	10380
374	tccggcctcc	gtgccatagg	agggcactcg	cgtgcctt	ctagcatgaa	gtgtgtgggg	10440
376	atttgacagaa	gcaacaggaa	acccatgcac	tgtgaatcta	ggattatttc	aaaacaaagg	10500
378	tttacagaaa	catccaagga	cagggctgaa	gtgcctccgg	gcaagggcag	ggcaggcacg	10560
380	agtgatttta	tttagctatt	ttattttatt	tacttacttt	ctgagacaga	gttatgctct	10620

## RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/995,419

TIME: 10:02:21

Input Set : A:\096,004 - SeqList.ST25.txt

Output Set : N:\CRF3\11212001\I995419.raw

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382 tgttgcccag gctggagtg agcgcatga tcttggetca ctgcaacctc cgtctcctgg 10680
384 gttcaagcaa ttctogtgcc tcagcctccc aagtagctgg gatttcaggc gtgcaccacc 10740
386 acacccggct aattttgtat ttttagtaga gatgggcttt caccatgttg gtcaggctga 10800
388 tctcaaaatc ctgacctcag gtgatccgcc cacctcagcc tcccaaagtg ctgggattac 10860
390 aggcattgag cactgcacct ggcctattta accattttta aacttccttg ggctcaagtc 10920
392 acacccactg gtaaggagtt catggagttc aatttccctt ttactcagga gttaccctcc 10980
394 tttgatattt tctgtaattc ttcgtagact ggggatacac cgtctcttga catattcaca 11040
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476 tccccttct ttccgcggcc ccgcccctc ctccgcggcg gattttcagg cagcgtctgc 13500
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/995,419

DATE: 12/05/2001

TIME: 10:02:22

Input Set : A:\096,004 - SeqList.ST25.txt

Output Set: N:\CRF3\11212001\I995419.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:546 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:548 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:548 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:555 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:557 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:557 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:564 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:566 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:566 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:573 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:575 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:575 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1420 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:1422 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:1422 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1429 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:1431 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:1431 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1438 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:1440 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:1440 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1470 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:1472 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:1472 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1485 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:1487 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:1487 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

<210> 2  
<211> 25  
<212> DNA  
<213> Artificial

requires <220> to <223>, please see  
error summary sheet, item ||

<400> 2  
cttgctgcag aagtgggtgg aggaa

25

<210> 3  
<211> 21  
<212> DNA  
<213> Artificial

<400> 3  
ctgcagtgtg ggtttcgggc a

21

<210> 4  
<211> 20  
<212> DNA  
<213> Artificial

<400> 4  
cggaagagtg tctggagcaa

20

<210> 5  
<211> 19  
<212> DNA  
<213> Artificial

<400> 5  
ggatgaagcg gagtctgga

19



<210> 14  
<211> 23  
<212> DNA  
<213> Artificial

— same

<400> 14  
ggcctgtact acatttgcct gga

23

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial

<400> 15  
gaaatagtgt caagtttcca tcacaa

26

<210> 16  
<211> 55  
<212> DNA  
<213> Artificial

<400> 16  
cgatgtggct gcggagccac cggcaggtaa tcctgttgat gctgattgtc tcaac

55

<210> 18  
<211> 17  
<212> PRT  
<213> Artificial

same

<400> 18

Met Trp Leu Arg Ser His Arg Gln Val Ile Leu Leu Met Leu Ile Val  
1 5 10 15

Ser

<210> 19  
<211> 17  
<212> PRT  
<213> Artificial

<400> 19

Met Trp Leu Arg Ser His Arg Gln Val Val Leu Ser Met Leu Leu Val  
1 5 10 15

Ser

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/995,419

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9 ✓      Use of n's or Xaa's  
    (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓      Use of <220>    Sequence(s) 2-5 14-16 <sup>18,19</sup> missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.